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QM protein nucleic search, using frame_plus.p2n model

Run on: January 16, 2003, 16:51:22 ; Search time 81 sec; Seconds
(without alignments)
137 557 Million cell updates/sec

Title: US-09-856-070-26

Perfect score: 28

Sequence: 1 query 5

Scoring table: BLOSUM62

Xgapop 10 0, Xgapext 0 5

Ygapop 10 0, Ygapext 0 5

Egapop 6 0, Egapext 7 0

Delop 6 0, Deloxt 7 0

Searched: 2185239 seqs, 115594019 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame_plus.p2n model -DEV=slp
-Q=/cgn2.1/pspro.spool/psoc65670/rusat_14012003_155833_1411/app_query.fasta_1502
-DB=N_Geneseq.101002 -GPMI=fastap -SUFFIX=mg -MINMATCH=0 -1-trunc=0
-LCPEXT=0 -UNITS=bits -SWAP=1 -FNU=1 -MATCH=1 -BLOSUM62 -USANS human.edi
-LIST=45 -LOCAL=200 -LHR=SLP -POT=1 -HR=MAX -LNU=2 -HR=MIN -ALIGN=15
-MODE=LOCAL -OUTFWT=ptlo -NRM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=PS0956670 -GNN=1.144K -TRIAL=14012003_155833_1411 -NFE=2 -1-10 3
-NO_XLPXY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT=1 -DYNHUG -DEV_TIMEOUT=16
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=5 -PCAPOP=6 -PCAPEXT=7
-YGAPOP=10 -YGAPEXT=5 -DELOP=6 -DELOXT=7

Database : N_Geneseq.101002.*

- 1: /SID82/gcdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SID82/gcdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SID82/gcdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SID82/gcdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SID82/gcdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SID82/gcdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SID82/gcdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SID82/gcdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SID82/gcdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SID82/gcdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SID82/gcdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SID82/gcdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SID82/gcdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SID82/gcdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SID82/gcdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SID82/gcdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SID82/gcdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SID82/gcdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SID82/gcdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SID82/gcdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SID82/gcdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SID82/gcdata/geneseq/geneseq-emb1/NA2001.DAT.*
- 23: /SID82/gcdata/geneseq/geneseq-emb1/NA2002.DAT.*
- 24: /SID82/gcdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	28	100.0	89	22	ABA70134
C 2	28	100.0	89	22	ABA70134
C 3	28	100.0	89	22	AAK18351
C 4	28	100.0	89	22	AAK44552
C 5	28	100.0	89	22	AAK150556
C 6	28	100.0	89	22	AAK18487
C 7	28	100.0	121	24	AAK25861
C 8	28	100.0	121	24	AAK25862
C 9	28	100.0	133	22	AAK59420
C 10	28	100.0	169	22	ABA66312
C 11	28	100.0	388	21	AAK10649
C 12	28	100.0	309	20	AAK98493
C 13	28	100.0	301	22	AAK66441
C 14	28	100.0	328	22	AAK55628
C 15	28	100.0	472	24	AFN19602
C 16	28	100.0	401	22	AAK96375
C 17	28	100.0	401	22	AAK97868
C 18	28	100.0	413	24	ABL27803
C 19	28	100.0	434	24	AAK57717
C 20	28	100.0	441	24	AAK96735
C 21	28	100.0	470	22	ABA57510
C 22	28	100.0	470	22	ABA26994
C 23	28	100.0	470	22	AAK05554
C 24	28	100.0	470	22	AAK31158
C 25	28	100.0	470	22	AAK37064
C 26	28	100.0	470	24	AAK05909
C 27	28	100.0	488	21	AAK03930
C 28	28	100.0	536	21	AAK38452
C 29	28	100.0	517	22	AAK37550
C 30	28	100.0	554	22	ABA64512
C 31	28	100.0	554	22	AAK38232
C 32	28	100.0	554	22	AAK14150
C 33	28	100.0	556	24	AAK18604
C 34	28	100.0	565	22	AAK6264
C 35	28	100.0	565	22	AAK09401
C 36	28	100.0	511	21	AAK51575
C 37	28	100.0	623	22	AAK05615
C 38	28	100.0	631	21	AAK51576
C 39	28	100.0	631	22	AAK06286
C 40	28	100.0	639	22	AAK06407
C 41	28	100.0	647	22	AAK46194
C 42	28	100.0	730	22	AAK43241
C 43	28	100.0	730	22	AAK43245
C 44	28	100.0	751	20	AAK98406
C 45	28	100.0	760	21	AAK16654

ALIGNMENTS

RESULT 1

ABA70134/C

IC ABA70134 standard; DNA: 89 BP.

XX ABA70134:

AC ABA70134:

XX 31 FEB 2002 (first entry)

XX Human fetal liver single exon nucleic acid probe #18439.

XX Human fetal liver, gene expression, single exon nucleic acid probe: ss.

XX Human sapiens.

XX W0200157277-A2.

XX 09-AUG-2001.

XX

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PR 30-JAN-2001; 2001W-US006669.
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000US-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WP1; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 4; SEQ ID NO 15380; 530pp; English.
XX the present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present human gene expression in a sample derived from human heart. The
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;

Alignment Scores:
Pred. No.: 104 Length: 89
Score: 28.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-070-26 (1-5) x ABA70134 (1-89)
OY 1 GluAspTyrGluGlu 5
DB 36 CAAGATTATGACAG 22
RESULT 2
ABA70134//
ID ABA70134 standard; DNA; 89 BP.
AC ABA70134;
XX ABA70134;
XX 24-JAN-2002 (first entry)
XX Probe #15380 for gene expression analysis in human heart cell sample.
XX Human: gene expression, heart, microarray, vascular system, probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001W-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000US-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WP1; 2001-48447/52.
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX Claim 4; SEQ ID NO 18439; 639pp + sequence listing; English.
XX the invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human fetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX fetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;

Alignment Scores:
Pred. No.: 104 Length: 89
Score: 28.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-856-070-26 (1-5) x ABA70134 (1-89)
OY 1 GluAspTyrGluGlu 5
DB 36 CAAGATTATGACAG 22
RESULT 2
ABA70134//
ID ABA70134 standard; DNA; 89 BP.
AC ABA70134;
XX ABA70134;
XX 24-JAN-2002 (first entry)
XX Probe #15380 for gene expression analysis in human heart cell sample.
XX Human: gene expression, heart, microarray, vascular system, probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.
XX Homo sapiens.
XX WO200157274-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001W-US00666.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000US-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WP1; 2001-488899/53.
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX Claim 4; SEQ ID NO 15380; 530pp; English.
XX the present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present human gene expression in a sample derived from human heart. The
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;

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XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DP WPI: 2001-488446/53.
 XX PT Single exon nucleic acid probes for analyzing gene expression in human
 XX PT brains -
 XX PS Example 4; SEQ ID NO: 18342; 650pp + Sequence Listing; English.
 XX CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 XX SQ Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;
 Alignment Scores:
 Pred. No.: 104 Length: 89
 Score: 28.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-070-26 (1-5) x AAK18351 (1-89)
 QY 1 GlnAspTyrGluGlu 5
 DB 36 CAAGATTATGAGAG 22
 RESULT 4
 AAK44252/C
 ID AAK44252 standard; DNA: 89 BP.
 AC AAK44252;
 XX 17-OCT-2001 (first entry)
 XX Probe #18942 used to measure gene expression in human placenta sample.
 XX Probe; microarray; human, placenta, antenatal diagnosis;
 XX genetic disorder; ss.
 XX Homo sapiens.
 XX W0200157272-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US006683.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0508408.
 XX 03-AUG-2000; 2000US-0532466.
 XX 21-SEP-2000; 2000US-0234487.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 XX Claim 25; SEQ ID No 18942; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENPs).
 XX The present sequence is one such probe. The probes are useful for
 XX producing a microarray for predicting, measuring and displaying gene
 XX expression in samples derived from human placenta. The probes are useful
 XX for antenatal diagnosis of human genetic disorders.
 XX Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;
 SQ

XX PS Example 4; SEQ ID NO: 18809; 658pp + Sequence Listing; English.
 XX CC the present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.
 XX SQ Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;
 Alignment Scores:
 Pred. No.: 104 Length: 89
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-856-070-26 (1-5) x AAK44252 (1-89)
 QY 1 GlnAspTyrGluGlu 5
 DB 36 CAAGATTATGAGAG 22
 RESULT 5
 AAK150256/C
 ID AAK150256 standard; DNA: 89 BP.
 XX AAK150256;
 XX 17-OCT-2001 (first entry)
 XX Probe #18942 used to measure gene expression in human placenta sample.
 XX Probe; microarray; human, placenta, antenatal diagnosis;
 XX genetic disorder; ss.
 XX Homo sapiens.
 XX W0200157272-A2.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US006683.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0508408.
 XX 03-AUG-2000; 2000US-0532466.
 XX 21-SEP-2000; 2000US-0234487.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human placenta -
 XX Claim 25; SEQ ID No 18942; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENPs).
 XX The present sequence is one such probe. The probes are useful for
 XX producing a microarray for predicting, measuring and displaying gene
 XX expression in samples derived from human placenta. The probes are useful
 XX for antenatal diagnosis of human genetic disorders.
 XX Sequence 89 BP; 22 A; 21 C; 16 G; 30 T; 0 other;
 SQ

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CC the array: identifying exons in a eukaryotic genome, comprising
CC (a) algorithmically predicting at least one exon from genomic sequences
CC of the eukaryote, and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene
CC expression analysis, and for identifying exons in a gene, particularly
CC using human lung derived mRNA and for the study of lung diseases
CC such as asthma, lung cancer, chronic obstructive pulmonary disease
CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
CC pulmonary alveolar proteinosis, Karagazer syndrome, fibrocystic
CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
CC and hyaline membrane disease. The present sequence is a single exon
CC probe open reading frame of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIP0 at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 89 bp; 22 A; 23 C; 16 G; 36 T; 0 other;
XX
Alignment Scores:
Prod. No.: 104 Length: 89
Score: 28.00 Matches: 5
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
XX
US-09-856-070-26 (1-5) x AHS18487 (1-89)
XX
QY 1 GlnAspTyrGluGlu 5
DB 36 CAAGATTATGAGAG 22
XX
RESULT 7
ABK25861/C
IL ABK25861 standard; LNA; 121 BP.
XX
AC AHS25861;
XX
DI 09-APR-2002 (first entry)
XX
DE Albino plant producing genome altering oligonucleotide #43.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW C methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine herbicide resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Lycopersicon esculentum.
XX Synthetic.
XX
PN WC200102512-A2.

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Alignment Scores:
Prod. No.: 104 Length: 89
Score: 28.00 Matches: 5
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
XX
US-09-856-070-26 (1-5) x AA150256 (1-89)
XX
QY 1 GlnAspTyrGluGlu 5
DB 36 CAAGATTATGAGAG 22
XX
RESULT 6
AHS18487/C
ID AHS18487 standard; DNA; 89 BP.
XX
AC AHS18487;
XX
DI 14-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 18478.
XX
KW Human, ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagazer syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
XX
PN WC200106003-A2.
XX
DI 15-NOV-2001.
XX
XX
XX 40-JAN-2001; 2001WO-0500665.
XX
XX 04-FEB-2000; 2000US-180412P.
XX
XX 26-MAY-2000; 2000US-207456P.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0642369.
XX
XX 21-SEP-2000; 2000US-234687P.
XX
XX 27-SEP-2000; 2000US-234659P.
XX
XX 04-OCT-2000; 2000GB-0044263.
XX
XX
XX (MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DK;
XX
XX WPI; 2002-114183/15.
XX
XX Spatially addressable set of single even nucleic acid probes, used to
XX measure gene expression in human lung samples -
XX
XX Claim 4: SEQ ID No 18478; 634pp; English.
XX
XX The invention relates to a spatially addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12487 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of
XX probes; the novel set of probes which hybridise at high stringency to a
XX nucleic acid expressed in the human lung; measuring gene expression in a
XX sample derived from human lung, comprising (a) contacting the array with
XX a collection of detectably labeled nucleic acids derived from human lung
XX mRNA, and (b) measuring the label detectably bound to each probe of

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XX 06-SEP-2001
 PD 01-JUN-2001: 2001WO-0817675
 PF 01-JUN-2000: 2000US-208538P
 PR 30-SEP-2000: 2000US-244989P
 PP 27-MAR-2001: 2001US-0818875
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmicc ER, Camper HB, Rice MC, Kim J;
 PI WPI: 2002-106307/14.
 XX
 DR New oligonucleotides with modified nuclease-resistant termini, useful
 PI for creating plants with desired phenotypes, e.g. stress tolerance,
 PT improved nutritional value, herbicide or disease resistance, or
 PI modified oil production
 XX
 PS Claim 7: Page 116: 220pp: English
 XX
 CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain, the DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an RNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.
 XX
 SQ Sequence 121 BP: 31 A: 21 C: 26 G: 43 T: 0 other;
 Alignment Scores:
 Pred. No.: 142 Length: 121
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-070-26 (1-5) x ABK25862 (1-121)
 QY 1 GlnAspTyrGluGlu 5
 DB 66 CAAGACTATGAGAA 52
 RESULT 8
 ABK25862
 ID ABK25862 standard; DNA: 121 BP.
 XX
 AC ABK25862;
 XX
 BI 09-APR-2002 (first entry)
 XX
 DE Albino plant producing genome altering oligonucleotide #34.
 XX
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; RNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration, environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.
 XX
 XX Lycopersicon esculentum.
 OS Synthetic.
 OS
 XX WC200192512-A2.
 XX
 XX 05-DEC-2001.
 XX
 XX 01-JUN-2001: 2001WO-US17672.
 XX
 XX 01-JUN-2000: 2000US-208538P.
 XX 20-OCT-2000: 2000US-244989P.
 XX 27-MAR-2001: 2001US-0818875.
 XX
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmicc ER, Camper HB, Rice MC, Kim J;
 PI WPI: 2002-106307/14.
 XX
 CC New oligonucleotides with modified nuclease-resistant termini, useful
 CC for creating plants with desired phenotypes, e.g. stress tolerance,
 CC improved nutritional value, herbicide or disease resistance, or
 CC modified oil production
 XX
 CC Claim 7: Page 116: 220pp: English.
 XX
 CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain, the DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an RNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention.
 XX
 SQ Sequence 121 BP: 43 A: 26 C: 21 G: 31 T: 0 other;
 Alignment Scores:
 Pred. No.: 142 Length: 121
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0
 US-09-856-070-26 (1-5) x ABK25862 (1-121)
 QY 1 GlnAspTyrGluGlu 5

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XX DE 56 CAACACTATGACGAA 70
XX RESULT 4
XX AAK50420/c
XX ID AAK50420 standard; DNA: 133 BP.
XX AC
XX AAK50420;
XX DE 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 24977.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN W0200157276 A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001W0-US00668.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000H4-0724247.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PN Penn SG, Hanzel DK, Chen W, Rank DK;
XX WP1: 2001-488900/53.
XX DE Human genome-derived single exon nucleic acid probes useful for
XX PT analyzing gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO: 24977; 658bp. Sequence listing, English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukemia and myeloma. The present sequence is one of
XX CC the probes of the invention.
XX SQ Sequence 133 BP: 28 A; 33 C; 17 G; 55 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 157 Length: 133
XX Score: 28.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US 09 856-070-26 (1-5) x AAK50420 (1-133)
XX
XX QY 1 GlnAspTyrGluGlu 5
XX AAF10649
XX ID AAF10649 standard; cDNA: 288 BP.
XX AC AAF10649;
XX AC
XX DI 13-MAR-2001 (first entry)
XX DE Fusarium venenatum PSI SEQ ID NO: 3172.
XX KW Multiple gene expression; filamentous fungal cell; EST;
XX KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX KW culture condition; environmental stress; spore morphogenesis;
XX KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX OS Fusarium venenatum.
XX PN W0200056762-A2.
XX DI 15-JAN-2002 (first entry)

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XX DE Soy bean SCN/SCS resistance related polynucleotide SEQ ID NO 90.
XX KW Soy bean; soybean cyst nematode; soybean; soybean cyst nematode; SCN/SCS;
XX KW transgenic plant; Heterodera glycines; Fusarium solani; ds.
XX OS Glycine max.
XX PN CA2331674-A1.
XX PD 28-JUL-2001.
XX PF 29-JAN-2001; 2001CA-2331674.
XX PR 28-JAN-2000; 2000US-0178811.
XX PA (UYSI-) UNIV SOUTHERN ILLINOIS.
XX PN Lightfoot DA, Meksem K;
XX WP1: 2001-590306/67.
XX PT Novel genetic marker associated with soybean cyst nematode or soybean
XX PT sudden death syndrome resistance in soybeans, used to produce resistant
XX PT cell lines and plants.
XX PS Disclosure; Page 183; 247pp; English.
XX CC The invention relates to genetic markers (AbA0624-AbA06344) associated
XX CC with soybean cyst nematode/soybean sudden death syndrome (SCN/SDS)
XX CC resistance in soybeans. The genetic markers provide for methods of
XX CC detecting SCN/SDS, for development of transgenic plant lines resistant to
XX CC SCN/SDS, especially the SCN Heterodera glycines but also Fusarium solani
XX CC and isolation of new genes and polypeptides able to provide resistance to
XX CC H. glycines and F. solani and substances which regulate the expression of
XX CC these genes.
XX SQ Sequence 160 BP: 43 A; 37 C; 32 G; 48 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 190 Length: 160
XX Score: 28.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 22 Gaps: 0
XX
XX US-09-856-070-26 (1-5) x ABA06312 (1-160)
XX
XX QY 1 GlnAspTyrGluGlu 5
XX AAF10649
XX ID AAF10649 standard; cDNA: 288 BP.
XX AC AAF10649;
XX AC
XX DI 13-MAR-2001 (first entry)
XX DE Fusarium venenatum PSI SEQ ID NO: 3172.
XX KW Multiple gene expression; filamentous fungal cell; EST;
XX KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
XX KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
XX KW culture condition; environmental stress; spore morphogenesis;
XX KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX OS Fusarium venenatum.
XX PN W0200056762-A2.
XX DI 15-JAN-2002 (first entry)

```

PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WV:US07981
 XX
 PR 22-MAR-1999; 980S-0273623
 XX
 PA (NOVO) NOVO NORDISK BIOFARM INC.
 PA (NOVO) NOVO NORDISK AS.
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 PI WPI: 2000-594572/56.
 DR
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags -
 XX
 PS Claim 86; Page 1511; 3161pp; English
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organization of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
 CC Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus
 CC niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and
 CC AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are
 CC all specifically claimed in the present invention.
 XX
 SQ Sequence 288 BP; 88 A; 49 C; 79 G; 70 T; 2 other;
 Alignment Scores:
 Pred. No... 346 Length. 288
 Score: 28.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 3
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Gaps: 0
 DB: 21
 US-09-856-070-26 (1-5) x AAF12949 (1 289)
 QY 1 GlnAspTyrGluGla 5
 AAX98493
 DB 4 CAAGATTACGAGAA 18
 RE-SUIT 12
 ID AAX98493 standard; cDNA: 300 BP.
 XX
 AC AAX98493;
 XX
 DT 24-SEP-1999 (first entry)
 XX
 DE Human cancer cell derived cDNA #219.
 XX
 KW Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
 KW integral membrane protein; aspartyl protease; GATA family; wnt family;
 KW transcription factor, G-protein alpha subunit, protein phosphatase;

phorbol ester binding protein, diacylglycerol binding protein; trypsin;
 protein kinase, tyrosine phosphatase, developmental signalling protein;
 WW/ist5/WWF domain, therapy, forensic, genetic mapping; diagnostic;
 detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
 Wilk's tumor; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
 leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
 prostate; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09933982-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 22-DEC-1998; 98WV-us27610.
 XX
 PR 21-DEC-1998; 98US-0217471
 PR 23-DEC-1997; 97US-0068755.
 PR 03-APR-1998; 98US-0040664
 PR 21-OCT-1998; 98US-0105234.
 PR 27-OCT-1998; 98US-0105877.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 CC Cravenjakov R, Dickson M, Drmanac R, Drmanac S;
 CC Escobedo V, Garcia PD, Garcia V, Giese K, Innis MA;
 CC Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
 CC Lamsan G, Leskowitz D, Pei D, Rabadanz F, Reichard C;
 CC Stache-Crain B, Sudduth-Klinger J, Williams LL;
 CC WPI: 1999-430243/36.
 XX
 CC New isolated human polynucleotides
 CC Claim 1; Page 370; 591pp; English.
 XX
 CC This invention describes novel isolated human polynucleotides obtained
 CC by screening for differential expression in colon cancer, breast cancer
 CC and lung cancer cell lines. The polynucleotides of the invention are
 CC represented in AAX98275-X99118 and encode polypeptides of protein
 CC families selected from 4 transmembrane segments integral membrane
 CC proteins, 7 transmembrane receptors, ATPases associated with various
 CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
 CC transcription factors, G protein alpha subunit, phospholipase or
 CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
 CC protein tyrosine phosphatase, trypsin, wnt family of developmental
 CC signalling proteins and WW/ist5/WWF domain containing proteins. The
 CC encoded polypeptides also have a functional domain selected from Ank
 CC repeat, basic region plus leucine zipper transcription factors,
 CC bromodomain, EF-hand, SH3 domain, WW domain, WW domain/3-belt repeats, zinc finger
 CC (C2H2 type), zinc finger (C2HC class), and zinc binding metalloprotease
 CC domain. The polynucleotides encode polypeptides with similarity to known
 CC protein families and are predicted to have similar properties. The novel
 CC polynucleotides can be used to develop products for use as therapeutic
 CC agents and in forensics, genetic analysis, mapping and diagnostic
 CC applications. In particular, the product can be used for the detection
 CC and management of cancers. They can be used for treating e.g. cervical
 CC cancers, melanomas, colorectal adenocarcinomas, Wilk's tumor, sarcomas,
 CC retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
 CC myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
 CC myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydric
 CC hereditary ectodermal dysplasia, congenital alveolar dysplasia,
 CC epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
 CC mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
 CC prostate or thyroid hyperplasias or pseudocarcinomatous hyperplasia of
 CC the skin.
 XX
 SQ Sequence 300 BP; 113 A; 55 C; 76 G; 56 T; 0 other;
 Alignment Scores:
 Pred. No.: 361 Length. 300
 Score: 28.00 Matches: 5

PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251040.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254047.
 PR 05-JAN-2001; 2001US-0250978.
 XX
 PA (HUMA-) HUMAN CHIMP SCI INC

XX
 PI Poser CA, Harash SC, Rubin SM.

XX
 DR WPI: 2001-463426/52

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PI useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.

XX
 PS Disclosure: SEQ ID NO 21253; 3071pp * Sequence listing: English.

CC AAK54951 to AAK64762 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC diagnosis and treat immune/hematopoietic related diseases, especially
 CC cancers and cancer metastases of hematopoietic derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genome
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK92160
 CC represent sequences used in the exemplification of the present invention.

XX
 SQ Sequence 301 BP; 68 A; 94 C; 71 G; 68 T; 0 other;

Alignment Scores:
 Pred. No.: 362 Length: 301
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservatives: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DH: 22 Gaps: 0

US-09-856-070-26 (1-5) x AAK66441 (1-301)

Oy 1 cInAspTyrGlycIn 5
 DB 57 CAGGACTAATGAACAA 71

RESULT 14

AAK55628
 ID AAK55628 standard; cDNA; 328 BP

XX

AC AAK55628;
 XX
 CT 06 NOV 2001 (first entry)
 XX
 DE Human immune/hematopoietic antigen encoding cDNA SEQ ID NO:688.
 XX
 KW Human, immune, hematopoietic, immune/hematopoietic antigen; cancer;
 KW cytostatic, gene therapy, vaccine, metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 IN W0200157182-A2.
 XX
 PS 09 AUG 2001.
 XX
 IT 17 JAN 2001, 2001WO-0501354.
 XX
 PR 31 JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180528.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-MAR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 24-JUL-2000; 2000US-0220963.
 PR 24-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0225779.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226968.
 PR 22-AUG-2000; 2000US-0227182.
 PR 24-AUG-2000; 2000US-0227099.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229369.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.

XX Homo sapiens.
 XX WO200192523-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US10836.
 XX 30-MAY-2000; 2000US-206132P.
 XX 29-AUG-2000; 2000US-238716P.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach MD:
 WPI: 2002-106308/14.
 P-PSDB: ABP03750.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 preventing and treating cardiovascular disease, neurodegenerative,
 hyperproliferative disorders and autoimmune disorders
 PS Disclosure; SEQ ID 7481; 1037pp; English.
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). AEN15762 to AEN27252 encode the human ORFX
 CC proteins given in APP00010 to APP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for aut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at http://wipo.int/pub/published_pat_sequences.
 XX Sequence 372 HP; 73 A; 125 C; 113 G; 59 T; 2 other;

Alignment Scores:
 Pred. No.: 450 Length: 372
 Score: 28.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-070-26 (1-5) x AEN19502 (1-372)

QY 1 GlnAspIyrGluGlu 5
 |||
 Db 84 CAGGACTACGAGAA 70

Search completed: January 16, 2003, 17:19:53
 Job time : 82.9821 secs

